



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hilton, Douglas J.
- (ii) TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 - (B) STREET: 400 Garden City Plaza
 - (C) CITY: Garden City
 - (D) STATE: New York
 - (E) COUNTRY: United States of America
 - (F) ZIP: 11530
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/702,665
 - (B) FILING DATE: 20-DEC-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Presser, Leopold
 - (B) REGISTRATION NUMBER: 19,827
 - (C) REFERENCE/DOCKET NUMBER: 10296
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (516) 742-4343
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 - (C) TELEX: 203 901 SANS UR

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 3..3
 - (D) OTHER INFORMATION: /note= "Xaa at Position 3 is any amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ser Xaa Trp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 45..1340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGAGGGTGA GGGCGGAGGC CGCTGGCGGC GGCTGCCGCA GAAG ATG AGC AGC AGC	56
Met Ser Ser Ser	
1	
TGC TCA GGG CTG ACC AGG GTC CTG GTG GCC GTG GCT ACA GCC CTG GTG	104
Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala Thr Ala Leu Val	
5 10 15 20	
TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG GGT CCT CCA GGG GTC CAG	152
Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gln	
25 30 35	
TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG TGC TGC CCC GGA GTG AGT	200
Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser	
40 45 50	
GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT GGA GAT TCA AGG CTG CTC	248
Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu	
55 60 65	
CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA CTG GTC TTG GCC CAG GTG	296
Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln Val	
70 75 80	
GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC CAG ACC CTG GAT GGT GTA	344
Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val	
85 90 95 100	
TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC TTT CCC CCA GCA CGT CCT	392
Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg Pro	
105 110 115	
GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA AAC TTC TCC TGT ACT TGG	440
Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr Trp	
120 125 130	

AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC CGC TAC CTT ACT TCC TAC Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr 135 140 145	488
AGG AAG AAG ACG CTG CCA GGA GCT GAG AGT CAG AGG GAA AGT CCA TCC Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro Ser 150 155 160	536
ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT CTG GAG GCC TCC CGA TGT Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys 165 170 175 180	584
GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG TAC CGG ATC AAT GTG ACC Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr 185 190 195	632
GAG GTG AAC CCA CTG GGT GCC AGC ACG TGC CTA CTG GAT GTG AGA TTA Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu Asp Val Arg Leu 200 205 210	680
CAG AGC ATC TTG CGT CCT GAT CCA CCC CAA GGA CTG CGG GTG GAA TCC Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser 215 220 225	728
GTA CCT GGT TAC CCG AGA CGC CTG CAT GCC AGC TGG ACA TAC CCT GCC Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp Thr Tyr Pro Ala 230 235 240	776
TCC TGG CGT CGC CAA CCC CAC TTT CTG CTC AAG TTC CGG TTG CAA TAC Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr 245 250 255 260	824
CGA CCA GCA CAG CAT CCA GCC TGG TCC ACG GTG GAG CCC ATT GGC TTG Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu Pro Ile Gly Leu 265 270 275	872
GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG CTG CCA CAC GCG GTA CGA Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro His Ala Val Arg 280 285 290	920
GTC AGT GCC AGG GAC TTT CTG GAT GCT GGC ACC TGG AGC GCC TGG AGC Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp Ser Ala Trp Ser 295 300 305	968
CCA GAG GCC TGG GGT ACT CCT AGC ACT GGT CCC CTG CAG GAT GAG ATA Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu Gln Asp Glu Ile 310 315 320	1016
CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG CTA GAG GCA GTA GTA GCT Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu Ala Val Val Ala 325 330 335 340	1064
CAG GAG GAC AGC CCG GCT CCT GCA AGG CCT TCC TTG CAG CCG GAC CCA Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro 345 350 355	1112
AGG CCA CTT GAT CAC AGG GAC CCC TTG GAG CAA GTA GCT GTG TTA GCG Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val Ala Val Leu Ala 360 365 370	1160

TCT CTG GGA ATC TTC TCT TGC CTT GGC CTG GCT GTT GGA GCT CTG GCA	1208
Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val Gly Ala Leu Ala	
375 380 385	
CTG GGG CTC TGG CTG AGG CTG AGA CGG AGT GGG AAG GAT GGA CCG CAA	1256
Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys Asp Gly Pro Gln	
390 395 400	
AAA CCT GGG CTC TTG GCA CCC ATG ATC CCG GTG GAA AAG CTT CCA GGA	1304
Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu Lys Leu Pro Gly	
405 410 415 420	
ATT CCA AAC CTG CAG AGG ACC CCA GAG AAC TTC AGC TGATTTTCATC	1350
Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser	
425 430	
TGTAACCCGG TCAGACTGGG GGCAGAAAGA GGCAGGGGCAG TGGATCCCTG TGGATGGAGG	1410
TCTCAGCTGA AAGTCTGAGC TCTTTTCTTT GACACCTATA CTCCAAACTT GCTGCCGGCT	1470
GAAGGCTGTC TGGACTTCCG ATGTCCTGAG GTGGAAGTCC ACCTGAGGAA TGTGTACAGA	1530
AGTCTGTGTT CCTGTGATCG TGTGTGTATG TGAGACAGGG AGCAAAAGTT CTCTGCATGT	1590
GTGTACAGAT GATTGGAGAG TGTGTGCGGT CTTGGGCTTG GCCCTTCTGG GAAGTGTGAA	1650
GAGTTGAAAT AAAAGAGACG GAAGTTTTTG GAAAAAAAAA AAAAAAAAAA AAAAA	1705

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Ser Ser Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala	
1 5 10 15	
Thr Ala Leu Val Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro	
20 25 30	
Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys	
35 40 45	
Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp	
50 55 60	
Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val	
65 70 75 80	
Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr	
85 90 95	

Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro
 100 105 110
 Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe
 115 120 125
 Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr
 130 135 140
 Leu Thr Ser Tyr Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg
 145 150 155 160
 Glu Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu
 165 170 175
 Ala Ser Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg
 180 185 190
 Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu
 195 200 205
 Asp Val Arg Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu
 210 215 220
 Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp
 225 230 235 240
 Thr Tyr Pro Ala Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe
 245 250 255
 Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu
 260 265 270
 Pro Ile Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro
 275 280 285
 His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp
 290 295 300
 Ser Ala Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu
 305 310 315 320
 Gln Asp Glu Ile Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu
 325 330 335
 Ala Val Val Ala Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu
 340 345 350
 Gln Pro Asp Pro Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val
 355 360 365
 Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val
 370 375 380
 Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys
 385 390 395 400
 Asp Gly Pro Gln Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu
 405 410 415

Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser
420 425 430

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 128..1396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTAACAGCC TTACCCCACT TGGTGCATCA ATTTTCTCTCC TAGGAAGCCT CAGTTTTGGA	60
GAGGAAGAGC CAGGCTTTAG CTCCCATCTC AGGGGTCGGG GATTTTGTGAC TCTACCTCTC	120
CCCACAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG GTG GCC	169
Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala	
1 5 10	
GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG GCC TGG	217
Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp	
15 20 25 30	
GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG AAG CTG	265
Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu	
35 40 45	
TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT CGG GAT	313
Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp	
50 55 60	
GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG CAT GAA	361
Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu	
65 70 75	
CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC ATC TGC	409
Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys	
80 85 90	
CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG CTG GGC	457
Gln Thr Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly	
95 100 105 110	

TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC TAT GAG	505
Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu	
115 120 125	
AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA CCC ACC	553
Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr	
130 135 140	
CGC TAC CTC ACC TCC TAC AGG AAG AAG ACA GTC CTA GGA GCT GAT AGC	601
Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser	
145 150 155	
CAG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG GAT CCC	649
Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro	
160 165 170	
CTA GGG GCT GCC CGC TGT GTT GTC CAC GGG GCT GAG TTC TGG AGC CAG	697
Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln	
175 180 185 190	
TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GGT GCC AGC ACA	745
Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Gly Ala Ser Thr	
195 200 205	
CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA CCC	793
Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro	
210 215 220	
CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA GGC CTG CGA	841
Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu Arg	
225 230 235	
GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC CTG	889
Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu	
240 245 250	
CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG TCC	937
Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser	
255 260 265 270	
ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG GCT	985
Thr Val Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala	
275 280 285	
GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT GCT	1033
Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala	
290 295 300	
GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC ACT	1081
Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr	
305 310 315	
GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG CAG	1129
Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln	
320 325 330	
CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC TCC	1177
Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser	

335	340	345	350	
CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG CAG				1225
Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln				
	355	360	365	
GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG GTG				1273
Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val				
	370	375	380	
GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG GGT GGG				1321
Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly				
	385	390	395	
AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA GTG				1369
Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val				
	400	405	410	
GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT				1416
Asp Arg Arg Pro Gly Ala Pro Asn Leu				
	415	420		
CGGCAGATTC CACCTATAAT CCTGTCTTGC TGGTGTGGAT AGAAACCAGG CAGGACAGTA				1476
GATCCCTATG GTTGGATCTC AGCTGGAAGT TCTGTTTGA GCCCATTTCT GTGAGACCCT				1536
GTATTTCAAA TTTGCAGCTG AAAGGTGCTT GTACCTCTGA TTTACCCCCA GAGTTGGAGT				1596
TCTGCTCAAG GAACGTGTGT AATGTGTACA TCTGTGTCCA TGTGTGACCA TGTGTCTGTG				1656
AAGCAGGGAA CATGTATTCT CTGCATGCAT GTATGTAGGT GCCTGGGGAG TGTGTGTGGG				1716
TCCTTGGCTC TTGGCCTTTC CCCTTGCAGG GGTGTGTGCAG GTGTGAATAA AGAGAATAAG				1776
GAAGTTCTTG GAGATTATAC TCAG				1800

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ser	Ser	Ser	Cys	Ser	Gly	Leu	Ser	Arg	Val	Leu	Val	Ala	Val	Ala
1				5					10					15	
Thr	Ala	Leu	Val	Ser	Ala	Ser	Ser	Pro	Cys	Pro	Gln	Ala	Trp	Gly	Pro
			20					25					30		
Pro	Gly	Val	Gln	Tyr	Gly	Gln	Pro	Gly	Arg	Ser	Val	Lys	Leu	Cys	Cys
		35					40					45			
Pro	Gly	Val	Thr	Ala	Gly	Asp	Pro	Val	Ser	Trp	Phe	Arg	Asp	Gly	Glu

50					55					60					
Pro	Lys	Leu	Leu	Gln	Gly	Pro	Asp	Ser	Gly	Leu	Gly	His	Glu	Leu	Val
65					70					75					80
Leu	Ala	Gln	Ala	Asp	Ser	Thr	Asp	Glu	Gly	Thr	Tyr	Ile	Cys	Gln	Thr
				85					90					95	
Leu	Asp	Gly	Ala	Leu	Gly	Gly	Thr	Val	Thr	Leu	Gln	Leu	Gly	Tyr	Pro
			100					105					110		
Pro	Ala	Arg	Pro	Val	Val	Ser	Cys	Gln	Ala	Ala	Asp	Tyr	Glu	Asn	Phe
		115					120					125			
Ser	Cys	Thr	Trp	Ser	Pro	Ser	Gln	Ile	Ser	Gly	Leu	Pro	Thr	Arg	Tyr
	130					135					140				
Leu	Thr	Ser	Tyr	Arg	Lys	Lys	Thr	Val	Leu	Gly	Ala	Asp	Ser	Gln	Arg
145					150					155					160
Arg	Ser	Pro	Ser	Thr	Gly	Pro	Trp	Pro	Cys	Pro	Gln	Asp	Pro	Leu	Gly
				165					170					175	
Ala	Ala	Arg	Cys	Val	Val	His	Gly	Ala	Glu	Phe	Trp	Ser	Gln	Tyr	Arg
			180					185					190		
Ile	Asn	Val	Thr	Glu	Val	Asn	Pro	Leu	Gly	Gly	Ala	Ser	Thr	Arg	Leu
	195						200					205			
Leu	Asp	Val	Ser	Leu	Gln	Ser	Ile	Leu	Arg	Pro	Asp	Pro	Pro	Gln	Gly
	210					215					220				
Leu	Arg	Val	Glu	Ser	Val	Pro	Gly	Tyr	Pro	Arg	Arg	Leu	Arg	Ala	Ser
225					230					235					240
Trp	Thr	Tyr	Pro	Ala	Ser	Trp	Pro	Cys	Gln	Pro	His	Phe	Leu	Leu	Lys
				245					250					255	
Phe	Arg	Leu	Gln	Tyr	Arg	Pro	Ala	Gln	His	Pro	Ala	Trp	Ser	Thr	Val
			260					265					270		
Glu	Pro	Ala	Gly	Leu	Glu	Glu	Val	Ile	Thr	Asp	Ala	Val	Ala	Gly	Leu
		275					280					285			
Pro	His	Ala	Val	Arg	Val	Ser	Ala	Arg	Asp	Phe	Leu	Asp	Ala	Gly	Thr
	290					295					300				
Trp	Ser	Thr	Trp	Ser	Pro	Glu	Ala	Trp	Gly	Thr	Pro	Ser	Thr	Gly	Thr
305					310					315					320
Ile	Pro	Lys	Glu	Ile	Pro	Ala	Trp	Gly	Gln	Leu	His	Thr	Gln	Pro	Glu
				325					330					335	
Val	Glu	Pro	Gln	Val	Asp	Ser	Pro	Ala	Pro	Pro	Arg	Pro	Ser	Leu	Gln
			340					345					350		
Pro	His	Pro	Arg	Leu	Leu	Asp	His	Arg	Asp	Ser	Val	Glu	Gln	Val	Ala
		355					360					365			

Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val Ala Gly
370 375 380

Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly Lys Asp
385 390 395 400

Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val Asp Arg
405 410 415

Arg Pro Gly Ala Pro Asn Leu
420

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "R at Position 1 is A or G"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /note= "Y at Position 7 is C or T"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /note= "R at Position 10 is A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

RCTCCAYTCR CTCCA

15

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..2

(D) OTHER INFORMATION: /note= "R at Position 1 is A or G"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 7..8

(D) OTHER INFORMATION: /note= "R at Position 7 is A or G"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 10..11

(D) OTHER INFORMATION: /note= "R at Position 10 is A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

RCTCCARTCR CTCCA

15

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..2

(D) OTHER INFORMATION: /note= "R at Position 1 is A or G"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 7..8

(D) OTHER INFORMATION: /note= "N at Position 7 is N"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 10..11

(D) OTHER INFORMATION: /note= "R at Position 10 is A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

RCTCCANGCR CTCCA

15

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..2

(D) OTHER INFORMATION: /note= "R at Position 1 is A or G"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 7..8

(D) OTHER INFORMATION: /note= "N at Position 7 is N"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 10..11

(D) OTHER INFORMATION: /note= "R at Position 10 is A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

RCTCCANGGR CTCCA

15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..2

(D) OTHER INFORMATION: /note= "R at Position 1 is A or G"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 7..8

(D) OTHER INFORMATION: /note= "Y at Position 7 is C or T"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 10..11

(D) OTHER INFORMATION: /note= "R at Position 10 is A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

RCTCCAYTTR CTCCA

15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGTCCACGG TGGAGCCCAT TGGCT 25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCACACGCGG TACGAGTCAG TGCCAGGGAC 30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCAAGTTCA GCCTGGTTAA G 21

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTATGAGTA TTTCTTCCAG GGTA 24

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCTTCATTG ACCTCAACTA CATG

24

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATGCCAGTG AGCTTCCCGT TCAG

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGTCCTCCA GGGGTCCAGT ATGG

24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGAGGCCTCC AGAGGGT

17

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCCTGTACT TGGAGTCCAG G

21

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAAAGCTGT GGC GTGATGG CCGTGGGGCA

30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGCGGAGGC CGCTGGCGGG CG

22

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTATCAGCTG AAGTTCTCTG GGG

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "R at Position 1 is G or A"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /note= "N at Position 7 is N"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /note= "R at Position 10 is G or A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

RCTCCANGCR CTCAA

15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCTTCTAGA TCCCCCTGCC CCCAAGCT

28

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ACTTTCTAGA TTATTGCTCC AAGGGGTCCC TGTG

34